

# 09433360 Results

SEQ ID NO: 2

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1819	100.0	350	20	AAY57290	Human BGCKr protei
2	1819	100.0	350	20	AAY17435	Human signal pepti
3	1819	100.0	350	20	AAW93169	Human HFIAO41 prot
4	1819	100.0	350	21	AAY94325	Human seven transm
5	1819	100.0	350	22	AAG80119	Human CCR11 protei
6	1819	100.0	350	22	AAU08994	Human G protein-co
7	1819	100.0	350	22	AAG67237	Amino acid sequenc
8	1819	100.0	382	22	AAB62389	Human chemokine re
9	1814	99.7	349	20	AAW93170	Human HFIAO41 prot
10	1814	99.7	350	20	AAY30125	A human seven-pass
11	1810	99.5	350	21	AAY71301	Human orphan G pro
12	1810	99.5	350	21	AAB02835	Human G protein co
13	1808	99.4	350	21	AAB37788	Human TSC7. Homo
14	1728	95.0	333	20	AAY57289	Human BGCKr partia
15	1620	89.1	350	22	AAG67238	Amino acid sequenc
16	1591	87.5	350	20	AAY57291	Mouse BGCKr protei
17	1275	70.1	246	20	AAY57292	Human BGCKr protei
18	1257	69.1	242	22	AAM99949	Human expressed po
19	1212	66.6	263	20	AAY30126	A seven-pass trans
20	862	47.4	164	22	ABB11162	Human orphan GPCR
21	862	47.4	164	22	AAM79310	Human protein SEQ
22	824	45.3	159	21	AAB41786	Human ORFX ORF1550
23	761	41.8	175	22	AAM99976	Human expressed po
24	761	41.8	175	22	ABB10276	Human cDNA SEQ ID
25	761	41.8	175	22	AAU18115	Novel human uterin
26	761	41.8	175	22	AAU18361	Human endocrine po
27	761	41.8	175	22	AAU18669	Renal and cardiova
28	761	41.8	175	22	AAU21655	Novel human neopla
29	659	36.2	358	15	AAR53745	Partial sequence o
30	659	36.2	358	21	AAB21689	Human 7TM receptor
31	659	36.2	378	19	AAW48724	Human V31 seven tr
32	659	36.2	378	21	AAB21688	Human 7TM receptor
33	659	36.2	378	22	AAG80114	Human CCR7 protein
34	659	36.2	378	22	AAB50859	Human CCR7. Homo
35	659	36.2	410	15	AAR53743	Putative seven tra
36	659	36.2	410	19	AAW48723	Polypeptide sequen
37	659	36.2	410	21	AAB21687	Genomic clone of 7
38	659	36.2	569	22	ABG12373	Novel human diagno
39	656	36.1	378	15	AAR53744	Putative seven tra
40	655	36.0	378	21	AAW90663	Human mutant G pro
41	653	35.9	378	21	AAY90629	Human G protein-co
42	650	35.7	378	21	AAB21699	7TM receptor prote
43	643	35.3	369	22	AAG80116	Human CCR9a protei
44	643	35.3	378	15	AAR54079	Epstein Barr virus
45	643	35.3	378	19	AAW56164	G-protein coupled

Issued:

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1819	100.0	350	2	US-08-966-316-16	Sequence 16, Appl
2	1620	89.1	350	2	US-08-966-316-18	Sequence 18, Appl
3	659	36.2	358	1	US-08-153-848-19	Sequence 19, Appl
4	659	36.2	358	3	US-09-299-843A-19	Sequence 19, Appl
5	659	36.2	358	4	US-09-088-337B-19	Sequence 19, Appl
6	659	36.2	358	5	PCT-US93-11153-19	Sequence 19, Appl

7	659	36.2	378	1	US-08-153-848-15	Sequence 15, Appl
8	659	36.2	378	3	US-09-299-843A-15	Sequence 15, Appl
9	659	36.2	378	4	US-09-251-545-1	Sequence 1, Appl
10	659	36.2	378	4	US-09-088-337B-15	Sequence 15, Appl
11	659	36.2	378	5	PCT-US93-11153-15	Sequence 15, Appl
12	659	36.2	410	1	US-08-153-848-7	Sequence 7, Appl
13	659	36.2	410	3	US-09-299-843A-7	Sequence 7, Appl
14	659	36.2	410	4	US-09-088-337B-7	Sequence 7, Appl
15	659	36.2	410	5	PCT-US93-11153-7	Sequence 7, Appl
16	650	35.7	378	3	US-09-299-843A-66	Sequence 66, Appl
17	650	35.7	378	4	US-09-088-337B-66	Sequence 66, Appl
18	643	35.3	378	1	US-08-383-750-2	Sequence 2, Appl
19	643	35.3	378	1	US-08-383-751A-2	Sequence 2, Appl
20	643	35.3	378	3	US-08-352-678-2	Sequence 2, Appl
21	643	35.3	378	4	US-09-045-583-49	Sequence 49, Appl
22	643	35.3	378	5	PCT-US93-09636-2	Sequence 2, Appl
23	637	35.0	357	4	US-09-266-464-2	Sequence 2, Appl
24	635.5	34.9	359	1	US-08-153-848-24	Sequence 24, Appl
25	635.5	34.9	359	3	US-09-299-843A-24	Sequence 24, Appl
26	635.5	34.9	359	4	US-09-088-337B-24	Sequence 24, Appl
27	635.5	34.9	359	5	PCT-US93-11153-24	Sequence 24, Appl
28	606.5	33.3	361	2	US-08-902-294-2	Sequence 2, Appl
29	606.5	33.3	361	3	US-09-178-637-2	Sequence 2, Appl
30	583	32.1	374	4	US-09-045-583-48	Sequence 48, Appl
31	581	31.9	342	4	US-09-116-498-4	Sequence 4, Appl
32	569	31.3	342	4	US-09-116-498-6	Sequence 6, Appl
33	560	30.8	342	2	US-08-742-011-2	Sequence 2, Appl
34	560	30.8	342	4	US-09-275-384B-5	Sequence 5, Appl
35	560	30.8	342	4	US-09-116-498-2	Sequence 2, Appl
36	560	30.8	342	4	US-09-449-437A-2	Sequence 2, Appl
37	537.5	29.5	360	4	US-08-875-573-20	Sequence 20, Appl
38	537.5	29.5	360	4	US-09-232-878-2	Sequence 2, Appl
39	537.5	29.5	360	4	US-09-045-583-55	Sequence 55, Appl
40	534.5	29.4	355	1	US-07-759-568-1	Sequence 1, Appl
41	534.5	29.4	355	1	US-08-450-393A-8	Sequence 8, Appl
42	534.5	29.4	355	2	US-08-390-000A-5	Sequence 5, Appl
43	534.5	29.4	355	4	US-08-446-669-8	Sequence 8, Appl
44	534.5	29.4	355	5	PCT-US95-00476-8	Sequence 8, Appl
45	534.5	29.4	360	1	US-08-202-056-7	Sequence 7, Appl

RESULT 1  
 US-08-966-316-16  
 ; Sequence 16, Application US/08966316  
 ; Patent No. 5932445  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Reddy, Roopa  
 ; APPLICANT: Murry, Lynn E.  
 ; APPLICANT: Mathur, Preete  
 ; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/966,316  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION: 435

*Slo ext*      *B*

; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0424 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 350 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: UTRSN0T11  
; CLONE: 2547002  
US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;  
Best Local Similarity 100.0%; Pred. No. 7.6e-148;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MALEQNQSTDYYYYENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
Db	1 MALEQNQSTDYYYYENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
Qy	61 MVVAIYAYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120
Db	61 MVVAIYAYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120
Qy	121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180
Db	121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180
Qy	181 NARCIPIFPRLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
Db	181 NARCIPIFPRLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
Qy	241 VLLTVVIVFIVTQLPYNIVKFCRAIDIYSLITSCNMSKRMEDIAIQVTE SIALFHSCLPN 300
Db	241 VLLTVVIVFIVTQLPYNIVKFCRAIDIYSLITSCNMSKRMEDIAIQVTE SIALFHSCLPN 300
Qy	301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPPFDSEGPTPEPTSTFSI 350
Db	301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPPFDSEGPTPEPTSTFSI 350

RESULT 2  
US-08-966-316-18  
; Sequence 18, Application US/08966316  
; Patent No. 5932445  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Reddy, Roopa  
; APPLICANT: Murry, Lynn E.  
; APPLICANT: Mathur, Preete  
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA

; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/966,316  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0424 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 18:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 350 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GenBank  
 ; CLONE: 399711  
 US-08-966-316-18

Query Match 89.1%; Score 1620; DB 2; Length 350;  
 Best Local Similarity 86.0%; Pred. No. 7.1e-131;  
 Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;  
  
 Qy 1 MALEQNQSTDYYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60  
 ||::|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||  
 Db 1 MAVEYNQSTDYYYYEENEMNDTHDYSQYEVICIKEEVRFKFAKVFPAFFTIAFIIGLAGNS 60  
  
 Qy 61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLFTLPFWAVNAVHGWLKGKIMCKITSALYT 120  
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||  
 Db 61 TVVVAIYAYYKKRRTKTDVYILNLAVADLFLLFTLPFWAVNAVHGWLKGKIMCKVTSALYT 120  
  
 Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||  
 Db 121 VNFVSGMQFLACISTDRYWAVTKAPSQSGVGKPCWVCFCVWAAILLSIPQLVFYTVNH 180  
  
 Qy 181 NARCIPIPPRLGTSKALIQMILEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240  
 ||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||  
 Db 181 KARCVPIFPYHLGTSMKASIQILEICIGFIIPFLIMAVCYFITAKTLIKMPNIKKSQPLK 240  
  
 Qy 241 VLLTVVVFIVTQLPYNIVKFCRAIDIYSLITSCNMSKRMEDIAIQTESIALFHSCLNP 300  
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||  
 Db 241 VLFTVVVFIVTQLPYNIVKFCQAIIDIYSLITDCDMSKRMEDIAIQITESIALFHSCLNP 300  
  
 Qy 301 ILYVFMGASFKNYVMKVAKKYGSWRQRQSVEEFPFDSEGPTEPSTFSI 350  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||  
 Db 301 VLYVFMGTSFKNYIMKVAKKYGSWRQRQNVEEIPFESEDATEPTSTFSI 350

#### SUMMARIES

%

Result	Query				
No.	Score	Match	Length	DB	ID

1	1620	89.1	350	2	JN0621	G protein-coupled
2	659	36.2	378	2	B55735	lymphocyte-specifi
3	650	35.7	378	2	A55735	G protein-coupled
4	643	35.3	378	2	A45680	G protein-coupled
5	583	32.1	369	2	JC5068	G protein-coupled
6	537.5	29.5	360	2	A57160	chemokine (C-C) re
7	534.5	29.4	360	2	A53611	interleukin-8 rece
8	524	28.8	354	2	I58186	probable G protein
9	522.5	28.7	355	2	JC4304	orphan G protein-c
10	522.5	28.7	360	2	JC4587	chemokine (C-C) re
11	518.5	28.5	354	2	B55733	G protein-coupled
12	511	28.1	358	2	A53752	interleukin-8 rece
13	501.5	27.6	355	2	JQ1231	interleukin-8 rece
14	500.5	27.5	352	2	A45747	neuropeptide Y/pep
15	499.5	27.5	353	2	S28787	neuropeptide Y/pep
16	493.5	27.1	352	2	G00048	fusin (LESTRA) - c
17	492	27.0	360	2	JC2443	chemokine (C-C) re
18	489.5	26.9	350	2	A39445	interleukin-8 rece
19	486	26.7	355	2	JC5067	G protein-coupled
20	485	26.7	355	2	I49339	macrophage inflamm
21	484.5	26.6	352	2	A43113	chemokine (C-C) re
22	483.5	26.6	359	2	A48921	interleukin-8 rece
23	482	26.5	374	2	I38450	chemokine (C-C) re
24	479.5	26.4	359	2	I49341	MIP-1 alpha recept
25	476.5	26.2	367	2	JE0349	interferon-inducib
26	474	26.1	355	2	A45177	chemokine (C-C) re
27	471	25.9	356	2	S42096	interleukin-8 rece
28	470	25.8	383	2	S55594	G protein-coupled
29	461.5	25.4	355	2	G02436	chemokine (C-C) re
30	455.5	25.0	359	2	S44425	angiotensin II rec
31	452.5	24.9	359	2	JC1104	angiotensin II rec
32	452.5	24.9	359	2	JC2134	angiotensin II rec
33	450	24.7	359	2	S15403	angiotensin II rec
34	450	24.7	374	2	S32785	G protein-coupled
35	446.5	24.5	359	2	A48857	angiotensin II rec
36	445.5	24.5	356	2	I49340	MIP-1 alpha recept
37	442.5	24.3	372	2	S26667	G protein-coupled
38	442.5	24.3	374	2	S42628	G protein-coupled
39	441	24.2	362	2	JN0694	angiotensin II rec
40	439	24.1	359	2	A42656	angiotensin II rec
41	438.5	24.1	359	2	JH0621	angiotensin II rec
42	438.5	24.1	362	2	A39714	G protein-coupled
43	437.5	24.1	327	2	S56162	MDCR15 protein - h
44	434	23.9	359	2	JQ1516	angiotensin II rec
45	428.5	23.6	359	2	I39418	angiotensin II rec

RESULT 1

JN0621

G protein-coupled receptor type B - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 19-May-2000

C;Accession: JN0621

R;Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.

Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A;Title: Identification of novel members of G-protein coupled receptor superfamily expressed in bovine taste tissue.

A;Reference number: JN0621; MUID:93326166

A;Accession: JN0621

A;Molecule type: mRNA

A;Residues: 1-350 <MAT>

A;Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711

A;Experimental source: tongue taste papillae

C;Comment: This protein is involved in modulating taste sensitivity or regeneration of taste cells.

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

F;42-66/Domain: transmembrane #status predicted <TM1>

F;80-99/Domain: transmembrane #status predicted <TM2>  
F;114-135/Domain: transmembrane #status predicted <TM3>  
F;154-175/Domain: transmembrane #status predicted <TM4>  
F;200-222/Domain: transmembrane #status predicted <TM5>  
F;242-265/Domain: transmembrane #status predicted <TM6>  
F;284-306/Domain: transmembrane #status predicted <TM7>  
F;6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.1%; Score 1620; DB 2; Length 350;  
Best Local Similarity 86.0%; Pred. No. 1.e-131;  
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

## SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	ID
1	1819	100.0	350	1	CKRB_HUMAN	Q9npb9 homo sapien
2	1620	89.1	350	1	CKRB_BOVIN	P35350 bos taurus
3	659	36.2	378	1	CKR7_HUMAN	P32248 homo sapien
4	650	35.7	378	1	CKR7_MOUSE	P47774 mus musculu
5	639	35.1	369	1	CKR9_MOUSE	Q9wut7 mus musculu
6	637	35.0	357	1	CKR9_HUMAN	P51686 homo sapien
7	605	33.3	367	1	CKR6_MOUSE	O54689 mus musculu
8	583	32.1	374	1	CKR6_HUMAN	P51684 homo sapien
9	581	31.9	342	1	CCR6_CERAE	O18983 cercopithec
10	571	31.4	343	1	CCR6_MACMU	Q9xt45 macaca mula
11	569	31.3	342	1	CCR6_MACNE	O19024 macaca neme
12	560	30.8	342	1	CCR6_HUMAN	O00574 homo sapien
13	537.5	29.5	360	1	CKR4_HUMAN	P51679 homo sapien
14	534.5	29.4	360	1	IL8B_HUMAN	P25025 homo sapien
15	529.5	29.1	353	1	IL8B_PANTR	Q28807 pan troglod
16	525	28.9	362	1	CKRA_HUMAN	P46092 homo sapien
17	524	28.8	354	1	C3X1_RAT	P35411 rattus norv
18	523	28.8	384	1	CKD6_HUMAN	O00590 homo sapien
19	522.5	28.7	353	1	IL8B_GORGO	Q28422 gorilla gor
20	522.5	28.7	355	1	C3X1_HUMAN	P49238 homo sapien
21	522.5	28.7	360	1	CKR4_MOUSE	P51680 mus musculu
22	521.5	28.7	353	1	IL8B_MACMU	Q28519 macaca mula
23	520.5	28.6	362	1	CKRA_MOUSE	Q9jl121 mus musculu
24	512	28.1	356	1	IL8B_CANFA	O97571 canis famil
25	511	28.1	354	1	C3X1_MOUSE	Q9z0d9 mus musculu
26	511	28.1	358	1	IL8B_RABIT	P35344 oryctolagus
27	504	27.7	360	1	CKR2_MACMU	O18793 macaca mula

28	501.5	27.6	355	1	IL8A_RABIT	P21109 oryctolagus
29	501.5	27.6	358	1	CKR3_CAVPO	Q9z2i3 cavia porce
30	500.5	27.5	352	1	CCR4_HUMAN	P30991 homo sapien
31	499.5	27.5	353	1	CCR4_BOVIN	P25930 bos taurus
32	499.5	27.5	360	1	IL8B_BOVIN	Q28003 bos taurus
33	498.5	27.4	352	1	CCR4_PAPAN	P56491 papio anubi
34	498.5	27.4	352	1	CKR5_CERTO	O62743 cercocebus
35	498.5	27.4	353	1	CCR4_FELCA	P56498 felis silve
36	497.5	27.4	350	1	IL8A_GORGO	P55919 gorilla gor
37	495.5	27.2	352	1	CKR5_CERAE	P56493 cercopithec
38	494.5	27.2	352	1	CCR4_CERTO	O62747 cercocebus
39	493.5	27.1	352	1	CCR4_MACFA	Q28474 macaca fasc
40	493.5	27.1	352	1	CCR4_MACMU	P79394 macaca mula
41	492.5	27.1	359	1	CKR3_RAT	O54814 rattus norv
42	492.5	27.1	359	1	IL8B_RAT	P35407 rattus norv
43	491.5	27.0	352	1	CKR5_PAPHA	P56441 papio hamad
44	491.5	27.0	352	1	CKR5_PYGBI	O97880 pygathrix b
45	490.5	27.0	352	1	CKR5_MACMU	P79436 macaca mula

#### ALIGNMENTS

RESULT 1  
 CKRB\_HUMAN  
 ID CKRB\_HUMAN STANDARD; PRT; 350 AA.  
 AC Q9NPB9;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 11 (C-C CKR-11) (CC-CKR-11) (CCR-11)  
 DE (Chemokine receptor-like 1) (CCRL1) (CCX CKR).  
 GN CCR11 OR CCPBP2 OR VSHK1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20200450; PubMed=10734104;  
 RA Schweickart V.L., Epp A., Raport C.J., Gray P.W.;  
 RT "CCR11 Is a functional receptor for the monocyte chemoattractant protein family of chemokines.";  
 RL J. Biol. Chem. 275:9550-9556 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20171478; PubMed=10706668;  
 RA Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z.,  
 RA Schall T.J.;  
 RT "Cutting edge: identification of a novel chemokine receptor that binds dendritic cell- and T cell-active chemokines including ELC, SLC, and TECK.";  
 RL J. Immunol. 164:2851-2856 (2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20231748; PubMed=10767544;  
 RA Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.,  
 RT "Cloning of CCRL1, an orphan seven transmembrane receptor related to chemokine receptors, expressed abundantly in heart.";  
 RL Gene 246:229-238 (2000).  
 CC -!- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4.  
 CC SCYA19/MIP3B/ELC, SCYA21/SLC AND SCYA25/TECK.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART. LOWER  
 CC EXPRESSION IN LUNG, PANCREAS, SPLEEN, SMALL INTESTINE AND FETAL  
 CC TISSUES.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF193507; AAF61299.1; --.  
 DR EMBL; AF233281; AAF44751.1; --.  
 DR EMBL; AF110640; AAF59827.1; --.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRRHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 43 63 POTENTIAL.  
 FT DOMAIN 64 87 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 88 108 POTENTIAL.  
 FT DOMAIN 109 113 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 114 134 POTENTIAL.  
 FT DOMAIN 135 154 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 155 175 POTENTIAL.  
 FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 202 222 POTENTIAL.  
 FT DOMAIN 223 240 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 241 261 POTENTIAL.  
 FT DOMAIN 262 289 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 290 310 POTENTIAL.  
 FT DOMAIN 311 350 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 112 184 BY SIMILARITY.  
 SQ SEQUENCE 350 AA; 39913 MW; 8E26049D2D5757C8 CRC64;

Query Match 100.0%; Score 1819; DB 1; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-104;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 MALEQNQSTDYYYYENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60  
 |||||||  
 Db 1 MALEQNQSTDYYYYENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60  
  
 Qy 61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLFTLPFWAVNAVHGWLKGKIMCKITSALYT 120  
 |||||||  
 Db 61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLFTLPFWAVNAVHGWLKGKIMCKITSALYT 120  
  
 Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180  
 |||||||  
 Db 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180  
  
 Qy 181 NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240  
 |||||||  
 Db 181 NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240  
  
 Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIYYSLITSCNMSKRMEDIAIQVTE SIALFHSCLN P 300  
 |||||||  
 Db 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIYYSLITSCNMSKRMEDIAIQVTE SIALFHSCLN P 300  
  
 Qy 301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPPFDSEGPTPEPTSTFSI 350  
 |||||||  
 Db 301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPPFDSEGPTPEPTSTFSI 350

RESULT 2  
 CKRB\_BOVIN  
 ID CKRB\_BOVIN STANDARD PRT; 350 AA.  
 AC P35350;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C-C chemokine receptor type 11 (-C CKR-11) (CC-CKR-11) (CCR-11)  
DE (Possible gustatory receptor type B) (PPR1 protein).  
GN CCR11.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tongue;  
RX MEDLINE=93326166; PubMed=8392843;  
RA Matsuoka I., Mori T., Aoki J., Sato T., Kurihara K.;  
RT "Identification of novel members of G-protein coupled receptor  
superfamily expressed in bovine taste tissue.";  
RL Biochem. Biophys. Res. Commun. 194:504-511(1993).  
CC -!- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4.  
CC SCYA19/MIP3B/ELC, SCYA21/SLC AND SCYA25/TECK (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM  
CC PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN  
CC LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.  
CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; S63848; AAB27547.1; -.  
DR PIR; JN0621; JN0621.  
DR GCRDb; GCR\_0757; -.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPSN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
KW Phosphorylation.  
FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 42 66 1 (POTENTIAL).  
FT DOMAIN 67 79 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 80 99 2 (POTENTIAL).  
FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 114 135 3 (POTENTIAL).  
FT DOMAIN 136 153 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 154 175 4 (POTENTIAL).  
FT DOMAIN 176 199 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 200 222 5 (POTENTIAL).  
FT DOMAIN 223 241 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 242 265 6 (POTENTIAL).  
FT DOMAIN 266 283 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 284 306 7 (POTENTIAL).  
FT DOMAIN 307 350 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT DISULFID 112 184 BY SIMILARITY.  
SQ SEQUENCE 350 AA; 40008 MW; E46BF942F3919C82 CRC64;

Query Match 89.1%; Score 1620; DB 1; Length 350;  
Best Local Similarity 86.0%; Pred. No. 1.8e-92;  
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MALEQNQSTDYYYYENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60  
||:| |||||||:||| :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||



Db 1 MAVEYNQSTDYYEENEMNDTHDYSQYEVICIKEEVRKFAKVFLPAFFTIIFIAGLNS 60  
 Qy 61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120  
 ||||| :  
 Db 61 TVVAIYAYYKKRRTKTDVYILNLAVADLFLLFTLPFWAVNAVHGVLGKIMCKVTSALYT 120  
 Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180  
 :  
 Db 121 VNFVSGMQFLACISTDRYWAVTKAPSQSGVGKPCWVICFCVWAAILLSIPQLVFYTVNH 180  
 Qy 181 NARCIPIFPRYLGTSMKALIQMLEICIGFVVPLIMGVCYFITARTLMKMPNIKISRPLK 240  
 ||| : | :  
 Db 181 KARCVPIFPYHLGTSMKASIQILEICIGFIIPFLIMAVCYFITAKTLIKMPNIKKSQPLK 240  
 Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIYSLITSCNMSKRMEDIAIQVTESIALFHSCLPN 300  
 || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 241 VLFTVVIVFIVTQLPYNIVKFCQAIDIYSLITDCDMSKRMEDIAQITESIALFHSCLPN 300  
 Qy 301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDESGPTEPTSTFSI 350  
 :  
 Db 301 VLYVFMGTSFKNYIMKVAKKYGSWRRQRQNVEEIPFESEDATEPTSTFSI 350

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1596	87.7	350	11	Q924I3	Q924i3 mus musculu
2	912	50.1	221	11	Q9ESK1	Q9esk1 rattus norv
3	643	35.3	369	4	Q9UQQ6	Q9uqq6 homo sapien
4	611	33.6	367	11	Q9R1V0	Q9r1v0 mus musculu
5	586.5	32.2	368	13	O42444	O42444 oncorhynchus
6	578	31.8	343	6	Q9N0Z0	Q9n0z0 cercocebus
7	566.5	31.1	351	11	Q9EQ16	Q9eq16 mus musculu
8	566	31.1	343	6	Q9BDS6	Q9bds6 macaca fasciata
9	561.5	30.9	351	11	Q9ERH5	Q9erh5 mus musculu
10	560	30.8	342	4	Q9HCA5	Q9hca5 homo sapien
11	559	30.7	342	6	Q9TV16	Q9tv16 pan troglodytes
12	544	29.9	358	13	Q9PUA0	Q9pua0 acipenser ruber
13	534.5	29.4	360	11	Q91ZH4	Q91zh4 rattus norvegicus
14	527	29.0	384	4	Q96A02	Q96a02 homo sapien
15	520.5	28.6	358	13	Q9YGC3	Q9ygc3 xenopus laevis
16	516	28.4	355	11	Q9JLY8	Q9jly8 rattus norvegicus
17	507.5	27.9	347	6	Q9MZM1	Q9mzm1 eulemur macaco
18	507	27.9	357	13	O42445	O42445 oncorhynchus tshawytscha
19	506.5	27.8	347	6	Q9MZM7	Q9mzm7 callimico pictus
20	506.5	27.8	347	6	Q9MZM6	Q9mzm6 callicebus personatus
21	503.5	27.7	347	6	Q9MZN0	Q9mzn0 alouatta seniculus
22	503.5	27.7	352	6	Q9TV44	Q9tv44 cercopithecus aethiops
23	502.5	27.6	347	6	Q9MZP1	Q9mzp1 mandrillus sphinx
24	502.5	27.6	347	6	Q9MZM9	Q9mzm9 atelopus varius
25	502.5	27.6	347	6	Q9MZM8	Q9mzm8 callithrix jacchus
26	502.5	27.6	347	6	Q9MZM5	Q9mzm5 pithecia pithecia
27	500.5	27.5	347	6	Q9MZP6	Q9mzp6 presbytis obscurus
28	500.5	27.5	347	6	Q9MZN6	Q9mzn6 hylobates agilis
29	500.5	27.5	347	6	Q9MZN5	Q9mzn5 hylobates hoolock
30	500.5	27.5	347	6	Q9MZN2	Q9mzn2 pongida pygmaeus
31	500.5	27.5	347	6	Q9MZN1	Q9mzn1 gorilla gorilla
32	500.5	27.5	352	6	Q9TSQ8	Q9tsq8 cercopithecus talapoin
33	499.5	27.5	339	6	Q9TUR8	Q9tur8 cercopithecus torquatus
34	499.5	27.5	339	6	Q9TUR4	Q9tur4 mandrillus leucophaeus
35	499.5	27.5	347	6	Q9MZQ3	Q9mzq3 pygathrix nigripes
36	499.5	27.5	347	6	Q9MZQ2	Q9mzq2 rhinopithecus roxellana
37	499.5	27.5	347	6	Q9MZQ1	Q9mzq1 pygathrix brevicaudata
38	499.5	27.5	347	6	Q9MZQ0	Q9mzq0 pygathrix nemoralis
39	499.5	27.5	347	6	Q9MZP9	Q9mzp9 nasalis larvatus
40	499.5	27.5	347	6	Q9MZP8	Q9mzp8 colobus poliocephalus
41	499.5	27.5	347	6	Q9MZP5	Q9mzp5 presbytis pileatus
42	499.5	27.5	347	6	Q9MZP4	Q9mzp4 presbytis femoralis

43	499.5	27.5	347	6	Q9MZP3	Q9mzp3 presbytis e
44	499.5	27.5	347	6	Q9MZP2	Q9mzp2 mandrillus
45	499.5	27.5	347	6	Q9MZP0	Q9mzp0 macaca assa

#### ALIGNMENTS

RESULT 1  
**Q924I3**  
ID Q924I3 PRELIMINARY; PRT; 350 AA.  
AC Q924I3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE CHEMOKINE RECEPTOR CCR11.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RX MEDLINE=20519697; PubMed=11063828;  
RA Dorf M.E., Berman M.A., Tanabe S., Heesen M., Luo Y.;  
RT "Astrocytes express functional chemokine receptors.";  
RL J. Neuroimmunol. 111:109-121(2000).  
DR EMBL; AF306532; AAK81712.1; -.  
KW Receptor.  
SQ SEQUENCE 350 AA; 39530 MW; C5F7D9DC949CECCF CRC64;

Query Match 87.7%; Score 1596; DB 11; Length 350;  
Best Local Similarity 85.4%; Pred. No. 1.6e-133;  
Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;  
  
Qy 1 MALEQNQSTDYYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60  
Db 1 MALELNQSAEYYYYEENEMYTHDYSQYEVICIKEEVQRQFAKVFLPAFFTVAFVTGLAGNS 60  
  
Qy 61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWLKGKIMCKITSALYT 120  
Db 61 VVVAIYAYYKKQRTKTDVYILNLAVADLLLLTLPFWAVNAVHGWLKGKMMCKVTSLALYT 120  
  
Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180  
Db 121 VNFVSGMQFLACISIDRYWAITKAPSQSGAGRCPWIICCCVWMAAILLSIPQLVFYTVNQ 180  
  
Qy 181 NARCIPIFPRYLGTSMKALIQMLEICIGFVVFLIMGVCYFITARTLMKMPNIKISRPLK 240  
Db 181 NARCTPIFPHLGTSLKASIQMLEIGFVVFLIMGVCYASTARALIKMPNIKKSRPLR 240  
  
Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIYSLITSCNMSKRMEDIAIQVTESIALFHSCLPN 300  
Db 241 VLLAVVVVFIVTQLPYNVVKFCQAIDAIYLLITSCDMSKRMDFVAIQVTESIALFHSCLPN 300  
  
Qy 301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPSTFSI 350  
Db 301 ILYVFMGASFKNYIMKVAKKYGSWRRQRQNVEEIPFDSEGPTEPSSFTI 350

SEQ ID NO: 1

#### SUMMARIES

% Result Query							Description
No.	Score	Match	Length	DB	ID		
1	1915	97.8	1915	9	AF110640	AF110640 Homo sapi	
c 2	1827.8	93.4	170546	2	AC074296	AC074296 Homo sapi	

3	1827.8	93.4	178159	9	HSJ509I19	AL121834 Human DNA	
c	4	1825.8	93.2	162029	9	AC020632	
5	1813.8	92.6	2407	6	E30057	Homo sapi	
6	1799.8	91.9	2156	6	E30058	E30057 G protein c	
7	1671.4	85.4	1925	6	AX244232	E30058 G protein c	
8	1671.4	85.4	1925	9	AF193507	AX244232 Sequence	
9	1574.6	80.4	1839	6	AX244231	AF193507 Homo sapi	
10	1462.6	74.7	1637	6	AX041923	AX244231 Sequence	
11	1370.8	70.0	1388	6	AX244225	AX041923 Sequence	
12	1150	58.7	1150	6	AX244230	AX244225 Sequence	
13	1132	57.8	1147	6	AX113671	AX244230 Sequence	
14	1132	57.8	1147	6	AX203742	AX113671 Sequence	
15	1119.2	57.2	1147	6	AX113673	AX203742 Sequence	
16	1111.4	56.8	1113	6	AX239641	AX113673 Sequence	
17	1111.4	56.8	1113	9	AF233281	AX239641 Sequence	
18	1051.4	53.7	1053	6	AX239643	AF233281 Homo sapi	
19	1051.4	53.7	1053	6	AX244219	AX239643 Sequence	
20	961.2	49.1	2059	4	S63848	AX244219 Sequence	
21	961.2	49.1	2059	6	AX244221	S63848 G-protein c	
22	831	42.4	831	6	AX244223	AX244221 Sequence	
23	797	40.7	797	6	AX244229	AX244223 Sequence	
24	790.4	40.4	1138	10	AF306532	AX244229 Sequence	
25	604	30.8	604	6	AX244227	AF306532 Mus muscu	
26	481	24.6	481	6	AX244224	AX244227 Sequence	
27	447.4	22.8	665	10	AF090348	AX244224 Sequence	
28	374	19.1	374	6	AX244228	AF090348 Rattus no	
29	345.4	17.6	347	6	AX113681	AX244228 Sequence	
30	180.2	9.2	1631	10	AF121670	AX113681 Sequence	
31	169.2	8.6	1302	10	AB009369	AF121670 Rattus no	
32	169.2	8.6	1674	10	MSM222714	AB009369 Mus muscu	
33	166.2	8.5	1500	9	HSDNABLR2	AJ222714 Mus muscu	
34	166.2	8.5	1900	6	AR107241	X84702 H.sapiens B	
35	166.2	8.5	2058	6	AR107232	AR107241 Sequence	
36	166.2	8.5	2139	9	HUMEBI11CDN	AR107232 Sequence	
37	166.2	8.5	2160	6	AR107239	L31581 Human G pro	
38	166.2	8.5	2215	9	HUMEBI103	AR107239 Sequence	
c	39	166.2	8.5	133801	9	AC004585	L31584 Human G pro
40	166	8.5	1410	10	AB016031	AC004585 Homo sapi	
41	164.8	8.4	1186	9	HSA132337	AB016031 Mus muscu	
42	164.8	8.4	2462	9	AF145440	AJ132337 Homo sapi	
43	164.8	8.4	2544	9	AF145439	AF145440 Homo sapi	
44	164.8	8.4	2577	9	HSU45982	AF145439 Homo sapi	
c	45	164.8	8.4	176968	9	AC005669	U45982 Human G pro
						AC005669 Homo sapi	

#### SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB ID		
1	1958	100.0	1958	21	AAA27006	Human cDNA encodin	
2	1813.8	92.6	2407	20	AAX22557	Human HFIAO41 cDNA	
3	1800	91.9	1800	24	AAS98075	Human DNA for pote	
4	1799.8	91.9	2156	20	AAX22558	Human HFIAO41 cDNA	
5	1671.4	85.4	1925	22	AAH77722	Genomic clone of h	
6	1636.8	83.6	1660	20	AAX61288	Human signal pepti	
7	1574.6	80.4	1839	22	AAH77721	Consensusc DNA se	
8	1462.6	74.7	1637	21	AAC68722	Human TSC7 cDNA.	
9	1370.8	70.0	1388	22	AAH77715	Nucleotide sequenc	
10	1207.4	61.7	1232	20	AAZ90528	Human BGCKr protei	
11	1150	58.7	1150	22	AAH77720	Nucleotide sequenc	
12	1145.8	58.5	1150	20	AAX86674	DNA encoding a sev	
13	1132	57.8	1147	22	AAF57685	Human chemokine re	
14	1119.2	57.2	1147	22	AAF57686	Human chemokine re	
15	1111.4	56.8	1113	22	AAS14572	Human cDNA encodin	
16	1090	55.7	1130	20	AAZ90527	Human BGCKr partia	
c	17	1057.4	54.0	1059	24	AAS98091	Human DNA for pote
18	1051.4	53.7	1053	22	AAH77711	Nucleotide sequenc	
19	1041.8	53.2	1053	21	AAD01128	Human orphan G pro	
20	1041.8	53.2	1053	21	AAA46029	Human G protein co	

21	996.8	50.9	1001	21	AAC75995	Human ORFX ORF1550
22	961.2	49.1	2059	22	AAH77712	Nucleotide sequenc
23	831	42.4	831	22	AAH77713	EST related to hum
24	816	41.7	828	22	AAI99561	Human expressed po
25	797	40.7	797	22	AAH77719	Nucleotide sequenc
26	770.4	39.3	1053	20	AAZ90529	Mouse BGCKr protei
27	652	33.3	660	24	AAS98119	Human DNA for pote
28	604	30.8	604	22	AAH77717	Nucleotide sequenc
29	592.2	30.2	789	20	AAX86675	DNA encoding a sev
c 30	551.6	28.2	821	22	AAI99588	Human expressed po
c 31	551.6	28.2	821	22	ABA06498	Human cDNA SEQ ID
c 32	551.6	28.2	821	22	AAS28957	cDNA encoding for
c 33	551.6	28.2	821	22	AAS29590	Human endocrine po
c 34	551.6	28.2	821	22	AAS30190	DNA encoding rena
c 35	551.6	28.2	821	22	AAS34854	CDNA encoding nove
36	493	25.2	493	22	ABA08406	Human orphan GPCR
37	493	25.2	493	22	AAK52443	Human polynucleoti
38	481	24.6	481	22	AAH77714	Nucleotide sequenc
39	374	19.1	374	22	AAH77718	Nucleotide sequenc
40	225	11.5	415	22	AAK51459	Human polynucleoti
41	167.8	8.6	2160	15	AAQ66160	Putative seven tra
42	166.2	8.5	1137	21	AAA30632	Human G protein-co
43	166.2	8.5	1137	21	AAA30729	DNA encoding human
44	166.2	8.5	1710	23	AAS76560	DNA encoding novel
45	166.2	8.5	1900	15	AAQ66162	Partial coding seq

Issued:

#### SUMMARIES

%

Result No.	Query				Description
	Score	Match	Length	DB ID	
1	1636.8	83.6	1660	2 US-08-966-316-17	Sequence 17, Appl
2	166.2	8.5	1900	1 US-08-153-848-18	Sequence 18, Appl
3	166.2	8.5	1900	3 US-09-299-843A-18	Sequence 18, Appl
4	166.2	8.5	1900	4 US-09-088-337B-18	Sequence 18, Appl
5	166.2	8.5	1900	5 PCT-US93-11153-18	Sequence 18, Appl
6	166.2	8.5	2058	1 US-08-153-848-6	Sequence 6, Appli
7	166.2	8.5	2058	3 US-09-299-843A-6	Sequence 6, Appli
8	166.2	8.5	2058	4 US-09-088-337B-6	Sequence 6, Appli
9	166.2	8.5	2058	5 PCT-US93-11153-6	Sequence 6, Appli
10	166.2	8.5	2160	1 US-08-153-848-14	Sequence 14, Appl
11	166.2	8.5	2160	3 US-09-299-843A-14	Sequence 14, Appl
12	166.2	8.5	2160	4 US-09-088-337B-14	Sequence 14, Appl
13	166.2	8.5	2160	5 PCT-US93-11153-14	Sequence 14, Appl
14	164.8	8.4	2577	4 US-09-266-464-1	Sequence 1, Appli
15	164.6	8.4	2085	3 US-09-299-843A-65	Sequence 65, Appl
16	164.6	8.4	2085	4 US-09-088-337B-65	Sequence 65, Appl
17	159.8	8.2	2154	1 US-08-383-750-1	Sequence 1, Appli
18	159.8	8.2	2154	1 US-08-383-751A-1	Sequence 1, Appli
19	159.8	8.2	2154	3 US-08-352-678-1	Sequence 1, Appli
20	159.8	8.2	2154	5 PCT-US93-09636-1	Sequence 1, Appli
21	153.6	7.8	1317	1 US-08-153-848-45	Sequence 45, Appl
22	153.6	7.8	1317	3 US-09-299-843A-45	Sequence 45, Appl
23	153.6	7.8	1317	4 US-09-088-337B-45	Sequence 45, Appl
24	153.6	7.8	1317	5 PCT-US93-11153-45	Sequence 45, Appl
25	153.6	7.8	1737	1 US-08-202-056-4	Sequence 4, Appli
26	153.6	7.8	1737	1 US-08-076-093A-3	Sequence 3, Appli
27	153.6	7.8	1737	1 US-08-701-265-3	Sequence 3, Appli
28	153.6	7.8	1737	2 US-08-284-586-3	Sequence 3, Appli
29	153.6	7.8	1737	2 US-08-805-478-3	Sequence 3, Appli
30	153.6	7.8	1737	2 US-08-802-627A-3	Sequence 3, Appli
31	153.6	7.8	1737	2 US-08-801-238-3	Sequence 3, Appli
32	153.6	7.8	1737	2 US-08-801-228-3	Sequence 3, Appli
33	153.6	7.8	1737	3 US-09-104-296-3	Sequence 3, Appli
34	153.6	7.8	1737	5 PCT-US94-06380-2	Sequence 2, Appli
35	152.2	7.8	2751	1 US-08-153-848-23	Sequence 23, Appli
36	152.2	7.8	2751	3 US-09-299-843A-23	Sequence 23, Appli

37	152.2	7.8	2751	4	US-09-088-337B-23	Sequence 23, Appl
38	152.2	7.8	2751	5	PCT-US93-11153-23	Sequence 23, Appl
39	143	7.3	1161	1	US-08-153-848-31	Sequence 31, Appl
40	143	7.3	1161	5	PCT-US93-11153-31	Sequence 31, Appl
41	143	7.3	2254	1	US-08-153-848-27	Sequence 27, Appl
42	143	7.3	2254	3	US-09-299-843A-27	Sequence 27, Appl
43	143	7.3	2254	4	US-09-088-337B-27	Sequence 27, Appl
44	143	7.3	2254	5	PCT-US93-11153-27	Sequence 27, Appl
45	143	7.3	3119	3	US-09-299-843A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1  
 US-08-966-316-17  
; Sequence 17, Application US/08966316  
; Patent No. 5932445  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Reddy, Roopa  
; APPLICANT: Murry, Lynn E.  
; APPLICANT: Mathur, Preete  
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/966,316  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0424 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1660 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: UTRSNOT11  
; CLONE: 2547002  
 US-08-966-316-17

Query Match 83.6%; Score 1636.8; DB 2; Length 1660;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1649; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 67 tacaacagattggaggccatggcttggaggcagaaccagtcaacagattattatgagg 126  
 |||||||



```

Db 1087 |||||||GCTCTGCCTTGCTTGGATACATATGAATGATGCTTCCTCAAATAAAACATCTGCA 1146
Qy 1207 ttattctgaaactcaaatctcagacgcgtggtgcaacttataataagaatgggtgg 1266
Db 1147 TTATTCTGAAACTCAAATCTCAGACGCCGTGGTGCAACTTATAATAAGAATGGGTGG 1206
Qy 1267 gggagggggagaaataaaagccaagaagaggaaacaagataataatgtacaaaacatg 1326
Db 1207 GGGAGGGGGAGAAATAAAAGCCAAGAAGAGGAAACAAGATAATAATGTACAAAACATG 1266
Qy 1327 aaaataaaaatgaacaatataggaaaataattgtAACAGGATAACTCTG 1386
Db 1267 AAAATTAAAATGAACAATATAGGAAAATAATTGTAAACAGGATAAGTGAATAACACTCTG 1326
Qy 1387 ctgttaacgaagaagaggtttgtggtgataatttgttatctgtggcgagtggcttata 1446
Db 1327 CTGTAACGAAGAAGAGCTTGTGGTGATAATTGTATCTGGTGCAGTGGTGCCTATA 1386
Qy 1447 caaatctacacaagtgataaaaatgacacagaactatatacacatgtaccaatttcaa 1506
Db 1387 CAAATCTACACAAGTGTAAACAGAGAACTATATACACACATTGTACCAATTCAA 1446
Qy 1507 tttcctgggtttgacattatagtataattatgttaagatggaccattggggaaaactggg 1566
Db 1447 TTTCCTGGTTTGACATTATAGTATAATTATGTAAAGATGGAACCATTGGGAAACTGGG 1506
Qy 1567 tgaagggttacccaggaccactctgtaccatcttgcgtacttgcgtgaatttataataat 1626
Db 1507 TGAAGGGTACCCAGGACCCTCTGTACCATCTTGTAACTTCCTGTGAATTATAATAAT 1566
Qy 1627 ttcaaaaataaaacaagtt-aaaaaaaaacccactatgtctataagttaggccatctaaaac 1685
Db 1567 TTCAAAATAAAACAAGTTAAAAAAAAACCCACTATGCTATAAGTTAGGCCATCTAAAC 1626
Qy 1686 agattattaaagaggttcatgttaaaaggcat 1717
Db 1627 AGATTATTAAAGAGGTTCATGTTAAAAGGCAT 1658

```

#### SUMMARIES

%						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	804.4	41.1	853	9	AL561603	AL561603 AL561603
2	711.4	36.3	774	10	BI759971	BI759971 603044413
3	570.6	29.1	711	10	BE970160	BE970160 601680190
4	476.4	24.3	575	10	BI681904	BI681904 461411 MA
5	469.8	24.0	782	10	BG205105	BG205105 RST24524
6	443	22.6	455	9	AA401504	AA401504 zu63b06.r
7	422	21.6	617	9	BB618186	BB618186 BB618186
c 8	403.8	20.6	859	9	AL582766	AL582766 AL582766
c 9	401	20.5	413	9	AA400266	AA400266 zu63b06.s
c 10	387.2	19.8	414	9	AI131555	AI131555 qb82c10.x
c 11	366	18.7	376	12	AQ893256	AQ893256 HS_2036_B
12	324.4	16.6	328	10	H67224	H67224 yu65d06.rl
13	302	15.4	576	9	BB639357	BB639357 BB639357
c 14	252.6	12.9	296	9	AI769466	AI769466 wj14d04.x
15	244.6	12.5	369	9	AA050273	AA050273 mj14a03.r
16	244.6	12.5	489	9	AA014373	AA014373 mg84c12.r
17	244.6	12.5	839	9	AI322657	AI322657 mj14a03.y
18	240.4	12.3	577	10	BM490381	BM490381 pgp2n.pk0
19	240.4	12.3	624	10	BI067951	BI067951 pgf1n.pk0
c 20	237.4	12.1	239	9	AI382794	AI382794 tc08f01.x
c 21	223.4	11.4	533	9	AI979038	AI979038 wr69e11.x
22	218.8	11.2	402	10	BG996991	BG996991 PM4-HT116
23	215.2	11.0	501	9	BB242286	BB242286 BB242286
24	208.4	10.6	560	10	BI067954	BI067954 pgf1n.pk0
25	205.2	10.5	612	9	BB628736	BB628736 BB628736
26	204.6	10.4	243	9	AU058992	AU058992 AU058992

27	192.6	9.8	315	9	BB586661	BB586661	
28	187	9.6	243	9	AU058629	AU058629	
29	182.4	9.3	217	9	AA215577	AA215577	
30	182	9.3	528	9	AW985634	AW985634	
31	162.6	8.3	471	9	AW355490	AW355490	
32	162	8.3	650	9	BB634771	BB634771	
c 33	159	8.1	407	10	BE813859	BE813859	
c 34	152.6	7.8	429	10	BF887414	BF887414	
c 35	147.8	7.5	539	10	BG264784	BG264784	
	36	147	7.5	3005	11	AK019478	AK019478
c 37	141.4	7.2	328	9	AW190975	AW190975	
c 38	136	6.9	772	10	BG739963	BG739963	
	39	130	6.6	408	12	AQ484477	AQ484477
c 40	123.8	6.3	423	9	AW137019	AW137019	
	41	123.8	6.3	871	10	BI653693	BI653693
c 42	122.6	6.3	643	12	AG091667	AG091667	
c 43	118.4	6.0	525	9	AI758214	AI758214	
c 44	118	6.0	642	12	AQ114597	AQ114597	
c 45	117	6.0	573	12	AQ195230	AQ195230	

SEQ ID NO: 1 nucleotides 1-324

```

RESULT      1
US-08-966-316-17
; Sequence 17, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
;   APPLICANT: Lal, Preeti
;   APPLICANT: Au-Young, Janice
;   APPLICANT: Reddy, Roopa
;   APPLICANT: Murry, Lynn E.
;   APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/966,316
;   FILING DATE: Herewith
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-855-0555
;   TELEFAX: 650-845-4166
;   TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1660 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single

```

```

;      TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: UTRSNOT11
;   CLONE: 2547002
US-08-966-316-17

      Query Match      79.1%; Score 256.4; DB 2; Length 1660;
Best Local Similarity 99.6%; Pred. No. 2.6e-68;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy    67 tacaacagattggagccatggcttggagcagaaccagtcaacagattattatgagg 126
Db    7 TACAACAGATTGGAGCCATGGCTTGGAACAGAACAGTCAACAGATTATTATGAGG 66

Qy    127 aaaatgaaatgaatggcaacttatgactacagtcaaatatgaactgtatcaaagaag 186
Db    67 AAAATGAAATGAATGGCACTTATGACTACAGTCAATATGAACGTGATCTGTATCAAAGAAG 126

Qy    187 atgtcagagaatttgaaaaagtttcctccgtattcctcacaatagtttcgtcattt 246
Db    127 ATGTCAGAGAATTTCGAAAGTTTCCTCCCTGTATTCCCTCACAAATAGTTTCGTCAATTG 186

Qy    247 gacttgaggcaattccatggtagtgttgcattataaagaaaacagagaacca 306
Db    187 GACTTGAGGCAATTCCATGGTAGTGGCAATTATGCCTATTACAAGAAAAGAGAACCA 246

Qy    307 aaacagatgtgtacatcc 324
Db    247 AAACAGATGTGTACATCC 264

```

SEQ ID NO: 1 nucleotides 652-1890

```

RESULT 1
US-08-966-316-17
; Sequence 17, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749

```

; REFERENCE/DOCKET NUMBER: PF-0424 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1660 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: UTRSNOT11  
CLONE: 2547002  
US-08-966-316-17

Query Match 85.0%; Score 1053.4; DB 2; Length 1660;  
Best Local Similarity 99.8%; Pred. No. 6.3e-254;  
Matches 1065; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 gctaccttagAACATcaatgaaAGCATTcaaATGCTAGAGATCTGCATTGGATTG 60  
Db 592 GCTACCTAGGAACATCAATGAAAGCATTGATTCAAATGCTAGAGATCTGCATTGGATTG 651

Qy 61 tagtacccttcttattatgggggtgtactttatcacagcaaggacactcatgaaga 120  
Db 652 TAGTACCCCTTCTTATTATGGGGGTGTGCTACTTTATCACAGCAAGGACACTCATGAAGA 711

Qy 121 tgccaaacattaaaatctcgaccctaaaagtctgcacagtcgttatagtttca 180  
Db 712 TGCCAAACATTAAAATATCTCGACCCTAAAAGTTCTGCTCACAGTCGTTAGTTTCA 771

Qy 181 ttgtcaactcaactgccttataacattgtcaagtctgccgagccatagacatcatctact 240  
Db 772 TTGTCACTCAACTGCCTTATAACATTGTCAAGTTCTGCCGAGCCATAGACATCATCTACT 831

Qy 241 ccctgatcaccagctgcaacatgagcaaACGcatggacatcgccatccaAGTCACAGAAA 300  
Db 832 CCCTGATCACCACTGCCTAACATGAGCAAACGATGGACATGCCATCCAAGTCACAGAAA 891

Qy 301 gcatcgactcttcacagctgcctcaacccaaatcctttatgtttttatggggcatctt 360  
Db 892 GCATCGACTCTTCACAGCTGCCTCAACCCAAATCCTTTATGTTTTATGGGAGCATCTT 951

Qy 361 tcaaaaactacgttatgaaagtggcaagaaatatggtcctggagaagacagagacaaa 420  
Db 952 TCAAAAACTACGTTATGAAAGTGGCAAGAAATATGGGTCTGGAGAAGACAGAGACAAA 1011

Qy 421 gtgtggaggagttccctttgattctgagggtcctacagagccaaccagtacttttagca 480  
Db 1012 GTGTGGAGGAGTTCCCTTTGATTCTGAGGGTCTACAGAGCCAACCAGTACTTTAGCA 1071

Qy 481 tttaaaggtaaaactgctgcctttgcttgatcacatatgaatgatgatgcTTCCCTCA 540  
Db 1072 TTTAAAGGTAAAACCTGCTCTGCCTTTGCTTGATACATATGAATGATGCTTCCCTCA 1131

Qy 541 aataaaaacatctgcattattctgaaactcaaactcagacgcgtgggtcaacttataa 600  
Db 1132 AATAAAACATCTGCATTATTCTGAAACTCAAATCTCAGACGCCGTGGTTGCAACTTATAA 1191

Qy 601 taaaAGAATgggtggggaaaggggagaaaataaaAGCCAAGAAGAGGAAACAAGATAATA 660  
Db 1192 TAAAAGAATGGGTGGGGAAAGGGGGAGAAAATAAAAGCCAAGAAGAGGAAACAAGATAATA 1251

Qy 661 aatgtacaaaacatgaaaattaaaatgacaatataggaaaataattgtaacaggcataa 720  
Db 1252 AATGTACAAAACATGAAAATTAAAATGAACAATATAGGAAAATAATTGTAAACAGGCATAA 1311

Qy 721 gtgaataaacactctgtgtacgaaAGAGAGCTTGTGGTgataattttgtatctgggtt 780

Db 1312 GTGAATAACACTCTGCTGTAACGAAGAAGAGCTTGTGGTGATAATTTGTATCTTGGTT 1371  
Qy 781 gcagtggtgcttatacaaatctacacaagtgataaaatgacacagaactatacacaca 840  
|||  
Db 1372 GCAGTGGTGCTTATACAAATCTACACAAGTGATAAAATGACAGAGAACTATACACACA 1431  
Qy 841 ttgtaccaatttcaatttcgtttgacattatagtataattatgtaaagatggaacca 900  
|||  
Db 1432 TTGTACCAATTCAATTCCCTGGTTTGACATTATAGTATAATTATGTAAGATGGAACCA 1491  
Qy 901 ttggggaaaactgggtgaagggtacccaggaccactctgtacccatcttgtaacttcctg 960  
|||  
Db 1492 TTGGGGAAAATGGGTGAAGGGTACCCAGGACACTCTGTACCCTTTGTAACCTCCTG 1551  
Qy 961 tgaatttataataattcaaaataaaacaagtt-aaaaaaaaacccactatgtataagt 1019  
|||  
Db 1552 TGAATTTATAATAATTCAAAATAAACAAAGTTAAAAAAAAACCCACTATGCTATAAGT 1611  
Qy 1020 taggccatctaaaacagattattaaagaggttcatgttaaaaggcat 1066  
|||  
Db 1612 TAGGCCATCTAAACAGATTATTAAGAGGTTCATGTTAAAGGCAT 1658